

5'	9	18	27	36	45	54											
GGG	ACT	TCC	AGT	AGG	AGG	CGG	CAT	GTT	TGA	AAA	GTG	ATG	ACG	GTT	GAC	GTT	TGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	63	72	81	90	99	108											
TGA	TTT	TTG	ACT	TTG	CTT	GTA	GCT	GCT	CCC	CGA	ACT	CGC	CGT	CTT	CCT	GTC	GGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	117	126	135	144	153	162											
GGC	CGG	CAC	TGT	AGG	TGA	GCG	GCA	GAG	GAC	GGA	GGA	AGG	AAG	CCT	GCA	GAC	AGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	171	180	189	198	207	216											
CGC	CTT	CTC	CAT	CCC	AAG	GCG	GCG	GCA	GGT	GCC	GGG	ACG	CTG	GGC	CTG	GCG	GTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	225	234	243	252	261	270											
TTT	TCG	TCG	TGC	TCA	GCG	GTG	GGA	GGA	GGC	GGA	AGA	AAC	CAG	AGC	CTG	GGA	GAT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	279	288	297	306	315	324											
TAA	CAG	GAA	ACT	TCC	AAG	ATG	GAA	ACT	TTG	TCT	TTC	CCC	AGA	TAT	AAT	GTA	GCT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	333	342	351	360	369	378											
GAG	ATT	GTG	ATT	CAT	ATT	CGC	AAT	AAG	ATC	TTA	ACA	GGA	GCT	GAT	GGT	AAA	AAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
E	I	V	I	H	I	R	N	K	I	L	T	G	A	D	G	K	N

FIGURE 1A

387	CTC	ACC	AAG	AAT	GAT	CTT	TAT	CCA	AAT	CCA	AAG	CCT	GAA	GTC	TTG	CAC	ATG	ATC	432
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	L	T	K	N	D	L	Y	P	N	P	K	P	E	V	L	H	M	I	
441	TAC	ATG	AGA	GCC	TTA	CAA	ATA	GTA	TAT	GGA	ATT	CGA	CTG	GAA	CAT	TTT	TAC	ATG	486
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Y	M	R	A	L	Q	I	V	Y	G	I	R	L	E	H	F	Y	M	
495	ATG	CCA	GTG	AAC	TCT	GAA	GTC	ATG	TAT	CCA	CAT	TTA	ATG	GAA	GGC	TTC	TTA	CCA	540
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	M	P	V	N	S	E	V	M	Y	P	H	L	M	E	G	F	L	P	
549	TTC	AGC	AAT	TTA	GTT	ACT	CAT	CTG	GAC	TCA	TTT	TTG	CCT	ATC	TGC	CGG	GTG	AAT	594
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	F	S	N	L	V	T	H	L	D	S	F	L	P	I	C	R	V	N	
603	GAC	TTT	GAG	ACT	GCT	GAT	ATT	CTA	TGT	CCA	AAA	GCA	AAA	CGG	ACA	AGT	CGG	TTT	648
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	D	F	E	T	A	D	I	L	C	P	K	A	K	R	T	S	R	F	
657	TTA	AGT	GGC	ATT	ATC	AAC	TTT	ATT	CAC	TTC	AGA	GAA	GCA	TGC	CGT	GAA	ACG	TAT	702
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	L	S	G	I	I	N	F	I	H	F	R	E	A	C	R	E	T	Y	

FIGURE 1B

711	ATG	GAA	TTT	CTT	TGG	CAA	TAT	AAA	TCC	TCT	GCG	GAC	AAA	ATG	CAA	CAG	TTA	AAC	756
	M	E	F	L	W	Q	Y	K	S	S	A	D	K	M	Q	Q	L	N	
765	GCC	GCA	CAC	CAG	GAG	GCA	TTA	ATG	AAA	CTG	GAG	AGA	CTT	GAT	TCT	GTT	CCA	GTT	810
	A	A	H	Q	E	A	L	M	K	L	E	R	L	D	S	V	P		
819	GAA	GAG	CAA	GAA	GAG	TTC	AAG	CAG	CTT	TCA	GAT	GGA	ATT	CAG	GAG	CTA	CAA	CAA	864
	E	E	Q	E	E	F	K	Q	L	S	D	G	I	Q	E	L	Q	Q	
873	TCA	CTA	AAT	CAG	GAT	TTT	CAT	CAA	AAA	ACG	ATA	GTG	CTG	CAA	GAG	GGA	AAT	TCC	918
	S	L	N	Q	D	F	H	Q	K	T	I	V	L	Q	E	G	N	S	
927	CAA	AAG	AAG	TCA	AAT	ATT	TCA	GAG	AAA	ACC	AAG	CGT	TTG	AAT	GAA	CTA	AAA	TTG	972
	Q	K	K	S	N	I	S	E	K	T	K	R	L	N	E	L	K	L	
981	TCG	GTG	GTT	TCT	TTG	AAA	GAA	ATA	CAA	GAG	AGT	TTG	AAA	ACA	AAA	ATT	GTG	GAT	1026
	S	V	V	S	L	K	E	I	Q	E	S	L	K	T	K	I	V	D	

FIGURE 1C

1035	1044	1053	1062	1071	1080
TCT CCA GAG AAG TTA AAG AAT TAT AAA GAA AAA ATG AAA GAT ACG GTC CAG AAG					
S P E K L K N Y K E K M K D T V Q K					
1089	1098	1107	1116	1125	1134
CTT AAA AAT GCC AGA CAA GAA GTG GTG GAG AAA TAT GAA ATC TAT GGA GAC TCA					
L K N A R Q E V V E K Y E I Y G D S					
1143	1152	1161	1170	1179	1188
GTT GAC TGC CTG CCT TCA TGT CAG TTG GAA GTG CAG TTA TAT CAA AAG AAA ATA					
V D C L P S C Q L E V Q L Y Q K I					
1197	1206	1215	1224	1233	1242
CAG GAC CTT TCA GAT AAT AGG GAA AAA TTA GCC AGT ATC TTA AAG GAG AGC CTG					
Q D L S D N R E K L A S I L K E S L					
1251	1260	1269	1278	1287	1296
AAC TTG GAG GAC CAA ATT GAG AGT GAT GAG TCA GAA CTG AAG AAA TTG AAG ACT					
N L E D Q I E S D E S E L K K L K T					
1305	1314	1323	1332	1341	1350
GAA GAA AAT TCG TTC AAA AGA CTG ATG ATT GTG AAG AAG GAA AAA CTT GCC ACA					
E E N S F K R L M I V K K E K L A T					

FIGURE 1D

1359	1368	1377	1386	1395	1404
GCA CAA TTC AAA ATA AAT AAG AAG CAT GAA GAT GTT AAG CAA TAC AAA CGC ACA					
A Q F K I N K K H E D V K Q Y K R T					
1413	1422	1431	1440	1449	1458
GTA ATT GAG GAT TGC AAT AAA GTT CAA GAA AAA AGA GGT GCT GTC TAT GAA CGA					
V I E D C N K V Q E K R G A V Y E R					
1467	1476	1485	1494	1503	1512
GTA ACC ACA ATT AAT CAA GAA ATC CAA AAA ATT AAA CTT GGA ATT CAA CAA CTA					
V T T I N Q E I Q K I K I K L G I Q Q L					
1521	1530	1539	1548	1557	1566
AAA GAT GCT GCT GAA AGG GAG AAA CTG AAG TCC CAG GAA ATA TTT CTA AAC TTG					
K D A A E R E K L K S Q E I F L N L					
1575	1584	1593	1602	1611	1620
AAA ACT GCT TTG GAG AAA TAC CAC GAC GGT ATT GAA AAG GCA GCA GAG GAC TCC					
K T A A L E E K Y H D G I E K A A E D S					
1629	1638	1647	1656	1665	1674
TAT GCT AAG ATA GAT GAG AAG ACA GCT GAA CTG AAG AGG AAG ATG TTC AAA ATG					
Y A K I D E K T A E L K R K M F K M					

FIGURE 1E

1683	1692	1701	1710	1719	1728
TCA ACC TGA TTA ACA AAA TTA CAT GTC TTT TTG TAA ATG GCT TGC CAT CTT TTA					
S T *					
1737	1746	1755	1764	1773	1782
ATT TTC TAT TTA GAA AGA AAA GTT GAA GCG AAT GGA AGT ATC AGA AGT ACC AAA					
1791	1800	1809	1818	1827	1836
TAA TGT TGG CTT CAT CAG TTT TTA TAC ACT CTC ATA AGT AGT TAA TAA GAT GAA					
1845	1854	1863	1872	1881	1890
TTT AAT GTA GGC TTT TAT TAA TTT ATA ATT AAA ATA ACT TGT GCA GCT ATT CAT					
1899	1908	1917	1926	1935	1944
GTC TCT ACT CTG CCC CTT GTT GTT GTA AAT AGT TTG AGT AAA ACA AAA CTA GTT ACC					
1953	1962	1971			
TTT GAA ATA TAT ATA TTT TTT TCT GTT ACA AAA AA 3'					

FIGURE 1F

1	M	E	T	L	S	F	P	R	Y	N	V	A	E	I	V	I	H	I	R	N	K	I	L	T	G	A	D	G	K	N	GRIIP
1	M	E	T	L	S	F	P	R	Y	N	I	A	E	I	V	H	I	R	N	K	L	L	T	G	A	D	G	K	N	HW051	
31	L	T	K	N	D	L	Y	P	N	P	K	P	E	V	L	H	M	I	Y	M	R	A	L	Q	I	V	Y	G	I	R	GRIIP
31	L	S	K	S	D	F	L	P	N	P	K	P	E	V	L	Y	M	I	Y	M	R	A	L	Q	L	V	Y	G	V	R	HW051
61	L	E	H	F	Y	M	M	P	V	N	S	E	V	M	Y	P	H	L	M	E	G	F	L	P	F	S	N	L	V	T	GRIIP
61	L	E	H	F	Y	M	M	P	V	N	I	E	V	M	Y	P	H	I	M	E	G	F	L	P	V	S	N	L	F	F	HW051
91	H	L	D	S	F	L	P	I	C	R	V	N	D	F	E	T	A	D	I	L	C	P	K	A	K	R	T	S	R	F	GRIIP
91	H	L	D	S	F	M	P	I	C	R	V	N	D	F	E	I	A	D	I	L	Y	P	K	A	N	R	T	S	R	F	HW051
121	L	S	G	I	I	N	F	I	H	F	R	E	A	C	R	E	T	Y	M	E	F	L	W	Q	Y	K	S	S	A	D	GRIIP
121	L	S	G	I	I	N	F	I	H	F	R	E	T	C	L	E	K	Y	E	E	F	L	L	Q	N	K	S	S	V	D	HW051
151	K	M	Q	Q	L	N	A	A	H	Q	E	A	L	M	K	L	E	R	L	D	S	V	P	V	E	E	Q	E	E	F	GRIIP
151	K	I	Q	Q	L	S	N	A	H	Q	E	A	L	M	K	L	E	K	L	N	S	V	P	V	E	E	Q	E	E	F	HW051
181	K	Q	L	S	D	G	I	Q	E	L	Q	Q	S	L	N	Q	D	F	H	Q	K	T	I	V	L	Q	E	G	N	S	GRIIP
181	K	Q	L	K	D	D	I	Q	E	L	Q	H	L	L	N	Q	D	F	R	Q	K	T	T	L	L	Q	E	R	Y	T	HW051
211	Q	K	K	S	N	I	S	E	K	T	K	R	L	N	E	L	K	L	S	V	S	L	K	E	I	Q	E	S	L	GRIIP	
211	K	M	K	S	D	F	S	E	K	T	K	H	V	N	E	L	K	L	S	V	S	L	K	E	V	Q	D	S	L	HW051	

FIGURE 2A

241	K	T	K	I	V	D	S	P	E	K	L	K	N	Y	K	E	K	M	K	D	T	V	Q	K	L	K	N	A	R	Q	GRIIP
241	K	S	K	I	V	D	S	P	E	K	L	K	N	Y	K	E	K	M	K	D	T	V	Q	K	L	R	S	A	R	E	HW051
271	E	V	V	E	K	Y	E	I	Y	G	D	S	V	D	C	L	P	S	C	Q	L	E	V	Q	L	Y	Q	K	K	I	GRIIP
271	E	V	M	E	K	Y	D	I	Y	R	D	S	V	D	C	L	P	S	C	Q	L	E	V	Q	L	Y	Q	K	K	S	HW051
301	Q	D	L	S	D	N	R	E	K	L	A	S	I	L	K	E	S	L	N	L	E	D	Q	I	E	S	D	E	S	E	GRIIP
301	Q	D	L	A	D	N	R	E	K	L	S	S	I	L	K	E	S	L	N	L	E	G	Q	I	D	S	D	S	S	E	HW051
331	L	K	K	L	K	T	E	E	N	S	F	K	R	L	M	I	V	K	K	E	K	L	A	T	A	Q	F	K	I	N	GRIIP
331	L	K	K	L	K	T	E	E	N	S	L	I	R	L	M	T	L	K	K	E	R	L	A	T	M	Q	F	K	I	N	HW051
361	K	K	H	E	D	V	K	Q	Y	K	R	T	V	I	E	D	C	N	K	V	Q	E	K	R	G	A	V	Y	E	R	GRIIP
361	K	K	Q	E	D	V	K	Q	Y	K	R	T	M	I	E	D	C	N	K	V	Q	E	K	R	D	A	V	C	E	Q	HW051
391	V	T	I	N	Q	E	I	Q	K	I	K	L	G	I	Q	Q	L	K	D	A	A	E	R	E	K	L	K	S	Q	GRIIP	
391	V	T	A	I	N	Q	D	I	H	K	I	K	S	G	I	Q	Q	L	R	D	A	E	K	R	E	K	L	K	S	Q	HW051
421	E	I	F	L	N	L	K	T	A	L	E	K	Y	H	D	G	I	E	K	A	A	E	D	S	Y	A	K	I	D	E	GRIIP
421	E	I	L	V	D	L	K	S	A	L	E	K	Y	H	E	G	I	E	K	T	E	E	C	C	T	R	I	G	G	HW051	
451	K	T	A	E	L	K	R	K	M	F	K	M	S	T																GRIIP	
451	K	T	A	E	L	K	R	R	M	F	K	M	P	P																HW051	

FIGURE 2B

Tissue Category	Clone Count	Found in	Ab Abund	Pct Abund
Cardiovascular System	266190	4/68	4	0.0015
Connective Tissue	144645	1/47	2	0.0014
Digestive System	501101	3/148	4	0.0008
Embryonic Structures	106713	2/21	2	0.0019
Endocrine System	225386	1/53	1	0.0004
Exocrine Glands	254635	2/64	2	0.0008
Genitalia, Female	427284	3/106	3	0.0007
Genitalia, Male	448207	2/114	6	0.0013
Germ Cells	38282	1/5	1	0.0026
Hemic and Immune System	680277	15/159	20	0.0029
Liver	109378	0/35	0	0.0000
Musculoskeletal System	159280	0/47	0	0.0000
Nervous System	955753	2/19	2	0.0002
Pancreas	110207	1/24	1	0.0009
Respiratory System	390086	4/93	5	0.0013
Sense Organs	19256	1/8	1	0.0052
Skin	72292	0/15	0	0.0000
Stomatognathic System	12923	0/10	0	0.0000
Unclassified/Mixed	120926	3/13	5	0.0041
Urinary Tract	279062	2/64	2	0.0007
Totals	5321883	47/1292	6	0.0000

FIGURE 3A

Found in:

Library ID	Clone Count	Library Description	Ab Abund	Pct Abund
BMARTXR02	682	bone marrow tumor line, neuroblastoma, t/6-OHDA,	1	0.1466
TLYMUNT01	3669	T-lymphocytes, allogenic, 40-50M, untreated	3	0.0818
TBLYN0T01	3119	T-B lymphoblast line, leukemia, untreated	2	0.0641
U937NOT01	2067	monocyte line, histiocytic lymphoma, untreated	1	0.0484
BMARTXT03	2162	bone marrow tumor line, neuroblastoma, t/6-OHDA	1	0.0463
BMARTXT06	2787	bone marrow tumor line, neuroblastoma, untreated	1	0.0359
SPLNTUT02	3017	spleen tumor, Hodgkin's, 45M	1	0.0331
MCLDTXT04	3310	UCB, derived dendritic cells, t/PMA, Ionomycin	1	0.0302
THYMFET03	3577	thymus, fetal, M	1	0.0280
MYEPTXT01	3944	CML precursor line, K-562, 53F, t/5AZA 72 h	1	0.0254
SPLNFET02	7859	spleen, fetal, 23wM	1	0.0127
TLYMNOT08	9784	T-lymphocytes, allogenic anergic, t/OKT3 3 day	1	0.0102

Two pooled libraries, two normalized libraries, and one subtracted library are not shown.

FIGURE 3B

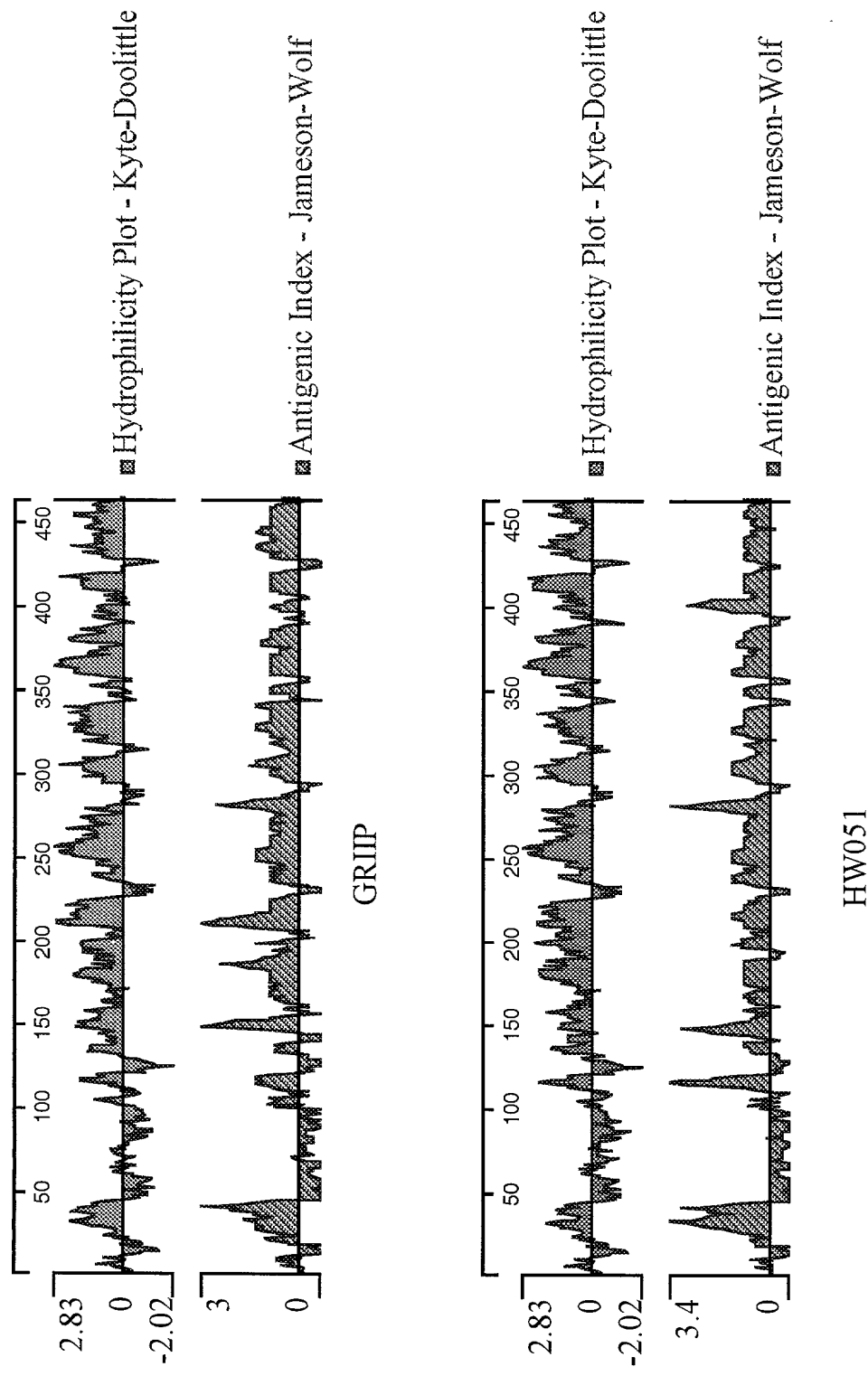


FIGURE 4